SEQUENCE LISTING

<110> Japan Science and Technology Agency
KURODA, Shunichi
TANIZAWA, Katsuyuki
KONDO, Akihiko
UEDA, Masakazu
SENO, Masaharu

<120> Hollow Protein Nanoparticles, and Drug Using the Same

<130> 1035-579 / P023P08US

<140> US 10/529,749
<141> 2005-03-30

<150> PCT/JP2003/015003
<151> 2003-11-25

<150> JP 2002-339925
<151> 2002-11-22

<160> 6

<170> MS Word

<210> 1
<211> 1218
<212> DNA
<213> Hepatitis B virus

<220>
<221> CDS
<222> (1)..(1218)

<400> 1

```
atg aga tct ttg ttg atc ttg gtt ttg tgt ttc ttg cca ttg gct gct   48
Met Arg Ser Leu Leu Ile Leu Val Leu Cys Phe Leu Pro Leu Ala Ala
  1               5                  10                  15

ttg ggt aag gtt cga caa ggc atg ggg acg aat ctt tct gtt ccc aat   96
Leu Gly Lys Val Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro Asn
             20                  25                  30

cct ctg gga ttc ttt ccc gat cac cag ttg gac cct gcg ttc gga gcc   144
Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala
         35                  40                  45

aac tca aac aat cca gat tgg gac ttc aac ccc aac aag gat caa tgg   192
Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp Gln Trp
     50                  55                  60

cca gag gca aat cag gta gga gcg gga gca ttc ggg cca ggg ttc acc   240
Pro Glu Ala Asn Gln Val Gly Ala Gly Ala Phe Gly Pro Gly Phe Thr
 65                  70                  75                  80
```

```
cca cca cac ggc ggt ctt ttg ggg tgg agc cct cag gct cag ggc ata   288
Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln Ala Gln Gly Ile
                 85                  90                  95

ttg aca aca gtg cca gca gca cct cct cct gcc tcc acc aat cgg cag   336
Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser Thr Asn Arg Gln
            100                 105                 110

tca gga aga cag cct act ccc atc tct cca cct cta aga gac agt cat   384
Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg Asp Ser His
        115                 120                 125

cct cag gcc atg cag tgg aat tcc aca aca ttc cac caa gct ctg cta   432
Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu
    130                 135                 140

gat ccc aga gtg agg ggc cta tat ttt cct gct ggt ggc tcc agt tcc   480
Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser
145                 150                 155                 160

gga aca gta aac cct gtt ccg act act gcc tca ccc ata tct ggg gac   528
Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Gly Asp
                165                 170                 175

cct gca ccg aac atg gag aac aca aca tca gga ttc cta gga ccc ctg   576
Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu
            180                 185                 190

ctc gtg tta cag gcg ggg ttt ttc ttg ttg aca aga atc ctc aca ata   624
Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
        195                 200                 205

cca cag agt cta gac tcg tgg tgg act tct ctc aat ttt cta ggg gga   672
Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
    210                 215                 220

gca ccc acg tgt cct ggc caa aat tcg cag tcc cca acc tcc aat cac   720
Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His
225                 230                 235                 240

tca cca acc tct tgt cct cca att tgt cct ggc tat cgc tgg atg tgt   768
Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys
                245                 250                 255

ctg cgg cgt ttt atc ata ttc ctc ttc atc ctg ctg cta tgc ctc atc   816
Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile
            260                 265                 270

ttc ttg ttg gtt ctt ctg gac tac caa ggt atg ttg ccc gtt tgt cct   864
Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro
        275                 280                 285

cta ctt cca gga aca tca acc acc agc acg ggg cca tgc aag acc tgc   912
Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys
    290                 295                 300
```

```
acg att cct gct caa gga acc tct atg ttt ccc tct tgt tgc tgt aca   960
Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr
305                 310                 315                 320

aaa cct tcg gac gga aac tgc act tgt att ccc atc cca tca tcc tgg   1008
Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp
                325                 330                 335

gct ttc gca aga ttc cta tgg gag tgg gcc tca gtc cgt ttc tcc tgg   1056
Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp
            340                 345                 350

ctc agt tta cta gtg cca ttt gtt cag tgg ttc gta ggg ctt tcc ccc   1104
Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro
        355                 360                 365

act gtt tgg ctt tca gtt ata tgg atg atg tgg tat tgg ggg cca agt   1152
Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser
    370                 375                 380

ctg tac aac atc ttg agt ccc ttt tta cct cta tta cca att ttc ttt   1200
Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe
385                 390                 395                 400

tgt ctt tgg gta tat att                                          1218
Cys Leu Trp Val Tyr Ile
                405
```

<210> 2
<211> 406
<212> PRT
<213> Hepatitis B virus

<400> 2

```
Met Arg Ser Leu Leu Ile Leu Val Leu Cys Phe Leu Pro Leu Ala Ala
  1               5                  10                  15

Leu Gly Lys Val Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro Asn
             20                  25                  30

Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala
         35                  40                  45

Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp Gln Trp
     50                  55                  60

Pro Glu Ala Asn Gln Val Gly Ala Gly Ala Phe Gly Pro Gly Phe Thr
 65                  70                  75                  80

Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln Ala Gln Gly Ile
                 85                  90                  95

Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser Thr Asn Arg Gln
            100                 105                 110
```

```
Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg Asp Ser His
        115                 120                 125

Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu
    130                 135                 140

Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser
145                 150                 155                 160

Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Gly Asp
                165                 170                 175

Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu
            180                 185                 190

Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
        195                 200                 205

Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
    210                 215                 220

Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His
225                 230                 235                 240

Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys
                245                 250                 255

Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile
            260                 265                 270

Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro
        275                 280                 285

Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys
    290                 295                 300

Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr
305                 310                 315                 320

Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp
                325                 330                 335

Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp
            340                 345                 350

Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro
        355                 360                 365

Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser
    370                 375                 380

Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe
385                 390                 395                 400

Cys Leu Trp Val Tyr Ile
                405
```

<210> 3
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 3
gccggtaccg cgagcttacc agttctc 27

<210> 4
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 4
gccctcgagg aaactaagtt tcttggt 27

<210> 5
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 5
gccctcgaga ccatggacat tgacccgtat 30

<210> 6
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 6
gccgagctcc taaacgcgtc cacattgaga ttcccgaga 39